

Title: US-10-666-513-2  
 Perfect score: 259  
 Sequence: 1 TKLEDHLEGIINIGHQYSVR.....ELKQLGTHKELPKTLQNXKDQ 50

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | Score | %<br>Query |        | DB | ID       | Description        |
|---------------|-------|------------|--------|----|----------|--------------------|
|               |       | Match      | Length |    |          |                    |
| 1             | 257   | 99.2       | 50     | 3  | AA90763  | Aay90763 Human EN- |
| 2             | 230   | 88.8       | 90     | 3  | AA90765  | Aay90765 Bovine CA |
| 3             | 230   | 88.8       | 90     | 3  | AA90764  | Aay90764 Bovine co |
| 4             | 230   | 88.8       | 92     | 2  | AA03563  | Aaw03563 Calcium b |
| 5             | 206   | 79.5       | 91     | 2  | AA01826  | Aaw01826 Component |
| 6             | 206   | 79.5       | 91     | 2  | AA93819  | Aaw93819 Angiotrop |
| 7             | 189   | 73.0       | 91     | 4  | AA31909  | Aab31909 Amino aci |
| 8             | 189   | 73.0       | 92     | 2  | AA03564  | Aaw03564 Calcium b |
| 9             | 189   | 73.0       | 92     | 2  | AA24137  | Aaw24137 Human che |
| 10            | 189   | 73.0       | 92     | 3  | AA45542  | Aab45542 Human S10 |
| 11            | 189   | 73.0       | 92     | 4  | AA31911  | Aab31911 Amino aci |
| 12            | 189   | 73.0       | 92     | 4  | AA31907  | Aab31907 Amino aci |
| 13            | 189   | 73.0       | 92     | 4  | AA31908  | Aab31908 Amino aci |
| 14            | 189   | 73.0       | 92     | 7  | AA93649  | Ada93649 Human cal |
| 15            | 189   | 73.0       | 92     | 8  | AD04192  | Adn04192 Antipsori |
| 16            | 189   | 73.0       | 92     | 8  | AD019540 | Ado19540 Human PRO |
| 17            | 174   | 67.2       | 95     | 4  | ABG27582 | Abg27582 Novel hum |
| 18            | 172   | 66.4       | 46     | 4  | ABB43183 | Abb43183 Peptide # |
| 19            | 172   | 66.4       | 46     | 4  | AAM37021 | Aam37021 Peptide # |
| 20            | 172   | 66.4       | 46     | 4  | ABB26281 | Abb26281 Protein # |

|    |     |      |     |   |           |          |           |
|----|-----|------|-----|---|-----------|----------|-----------|
| 21 | 172 | 66.4 | 46  | 4 | AAM76914  | Aam76914 | Human bon |
| 22 | 172 | 66.4 | 46  | 4 | AAM64093  | Aam64093 | Human bra |
| 23 | 172 | 66.4 | 46  | 4 | ABG58579  | Abg58579 | Human liv |
| 24 | 172 | 66.4 | 46  | 5 | ABG46027  | Abg46027 | Human pep |
| 25 | 139 | 53.7 | 30  | 2 | AAR85169  | Aar85169 | Bovine se |
| 26 | 114 | 44.0 | 112 | 7 | ADB79921  | Adb79921 | Rat intra |
| 27 | 114 | 44.0 | 112 | 7 | ADE57108  | Ade57108 | Rat Prote |
| 28 | 114 | 44.0 | 113 | 6 | ABU63335  | Abu63335 | Rat intra |
| 29 | 110 | 42.5 | 114 | 2 | AAW17062  | Aaw17062 | Human mul |
| 30 | 110 | 42.5 | 114 | 2 | AAW60178  | Aaw60178 | Human cal |
| 31 | 110 | 42.5 | 114 | 2 | AAAY48615 | Aay48615 | Human bre |
| 32 | 110 | 42.5 | 114 | 3 | AAAY87637 | Aay87637 | Human cal |
| 33 | 110 | 42.5 | 114 | 3 | AAB45539  | Aab45539 | Human S10 |
| 34 | 110 | 42.5 | 114 | 4 | ABB44613  | Abb44613 | Human wou |
| 35 | 110 | 42.5 | 114 | 4 | AAB31905  | Aab31905 | Amino aci |
| 36 | 110 | 42.5 | 114 | 6 | ABB82712  | Abb82712 | Human MRP |
| 37 | 110 | 42.5 | 114 | 7 | ADB17567  | Adb17567 | Human mye |
| 38 | 110 | 42.5 | 114 | 7 | ADE57110  | Ade57110 | Human Pro |
| 39 | 110 | 42.5 | 114 | 7 | ADE34548  | Ade34548 | Human mig |
| 40 | 110 | 42.5 | 114 | 7 | ADF09358  | Adf09358 | Human cal |
| 41 | 110 | 42.5 | 114 | 8 | ADL83164  | Adl83164 | Human PRO |
| 42 | 110 | 42.5 | 114 | 8 | ADN03968  | Adn03968 | Antipsori |
| 43 | 110 | 42.5 | 114 | 8 | ADQ30562  | Adq30562 | Pancreas  |
| 44 | 110 | 42.5 | 115 | 4 | AAB31930  | Aab31930 | Amino aci |
| 45 | 110 | 42.5 | 152 | 4 | AAM39994  | Aam39994 | Human pol |

Title: US-10-666-513-2  
 Perfect score: 259  
 Sequence: 1 TKLEDHLEGIINIGHQYSVR.....ELKQLGTHKELPKTLQNXKDQ 50

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Query |        | DB | ID                  | Description       |
|------------|-------|---------|--------|----|---------------------|-------------------|
|            |       | Match   | Length |    |                     |                   |
| 1          | 257   | 99.2    | 50     | 4  | US-09-263-312-2     | Sequence 2, Appli |
| 2          | 257   | 99.2    | 50     | 4  | US-09-826-589-2     | Sequence 2, Appli |
| 3          | 230   | 88.8    | 51     | 2  | US-08-568-310D-2    | Sequence 2, Appli |
| 4          | 230   | 88.8    | 51     | 3  | US-09-270-455-2     | Sequence 2, Appli |
| 5          | 230   | 88.8    | 90     | 4  | US-09-263-312-3     | Sequence 3, Appli |
| 6          | 230   | 88.8    | 90     | 4  | US-09-826-589-3     | Sequence 3, Appli |
| 7          | 230   | 88.8    | 90     | 4  | US-09-826-589-4     | Sequence 4, Appli |
| 8          | 230   | 88.8    | 92     | 2  | US-08-568-310D-19   | Sequence 19, Appl |
| 9          | 230   | 88.8    | 92     | 3  | US-09-270-455-19    | Sequence 19, Appl |
| 10         | 206   | 79.5    | 91     | 3  | US-08-794-000-2     | Sequence 2, Appli |
| 11         | 206   | 79.5    | 91     | 4  | US-09-646-651C-1    | Sequence 1, Appli |
| 12         | 189   | 73.0    | 92     | 2  | US-08-568-310D-20   | Sequence 20, Appl |
| 13         | 189   | 73.0    | 92     | 3  | US-09-270-455-20    | Sequence 20, Appl |
| 14         | 114   | 44.0    | 113    | 2  | US-08-918-727-7     | Sequence 7, Appli |
| 15         | 114   | 44.0    | 113    | 3  | US-09-205-680A-7    | Sequence 7, Appli |
| 16         | 110   | 42.5    | 50     | 1  | US-08-200-016-5     | Sequence 5, Appli |
| 17         | 110   | 42.5    | 109    | 1  | US-07-987-272A-8    | Sequence 8, Appli |
| 18         | 110   | 42.5    | 114    | 1  | US-08-385-241-3     | Sequence 3, Appli |
| 19         | 110   | 42.5    | 114    | 4  | US-09-214-272-4     | Sequence 4, Appli |
| 20         | 110   | 42.5    | 114    | 4  | US-09-806-382A-4    | Sequence 4, Appli |
| 21         | 87    | 33.6    | 74     | 4  | US-09-513-999C-5490 | Sequence 5490, Ap |
| 22         | 87    | 33.6    | 95     | 4  | US-09-919-172-102   | Sequence 102, App |

|    |    |      |     |   |                     |                   |
|----|----|------|-----|---|---------------------|-------------------|
| 23 | 87 | 33.6 | 95  | 4 | US-09-976-594-467   | Sequence 467, App |
| 24 | 84 | 32.4 | 91  | 1 | US-07-987-272A-11   | Sequence 11, Appl |
| 25 | 84 | 32.4 | 92  | 2 | US-08-918-727-5     | Sequence 5, Appli |
| 26 | 84 | 32.4 | 92  | 2 | US-09-051-589-1     | Sequence 1, Appli |
| 27 | 84 | 32.4 | 92  | 3 | US-09-205-680A-5    | Sequence 5, Appli |
| 28 | 84 | 32.4 | 92  | 4 | US-09-919-039-184   | Sequence 184, App |
| 29 | 83 | 32.0 | 101 | 1 | US-08-190-560-2     | Sequence 2, Appli |
| 30 | 83 | 32.0 | 101 | 1 | US-08-469-277-2     | Sequence 2, Appli |
| 31 | 83 | 32.0 | 101 | 2 | US-08-468-946-2     | Sequence 2, Appli |
| 32 | 83 | 32.0 | 101 | 2 | US-08-468-942-2     | Sequence 2, Appli |
| 33 | 83 | 32.0 | 101 | 4 | US-09-298-625-2     | Sequence 2, Appli |
| 34 | 75 | 29.0 | 45  | 1 | US-08-056-200-98    | Sequence 98, Appl |
| 35 | 75 | 29.0 | 45  | 2 | US-08-800-644-98    | Sequence 98, Appl |
| 36 | 75 | 29.0 | 107 | 4 | US-09-513-999C-5491 | Sequence 5491, Ap |
| 37 | 74 | 28.6 | 45  | 1 | US-08-056-200-101   | Sequence 101, App |
| 38 | 74 | 28.6 | 45  | 2 | US-08-800-644-101   | Sequence 101, App |
| 39 | 74 | 28.6 | 47  | 1 | US-08-200-016-2     | Sequence 2, Appli |
| 40 | 74 | 28.6 | 93  | 1 | US-07-987-272A-7    | Sequence 7, Appli |
| 41 | 74 | 28.6 | 93  | 1 | US-07-987-272A-16   | Sequence 16, Appl |
| 42 | 74 | 28.6 | 93  | 1 | US-08-385-241-1     | Sequence 1, Appli |
| 43 | 74 | 28.6 | 93  | 4 | US-09-214-272-2     | Sequence 2, Appli |
| 44 | 74 | 28.6 | 93  | 4 | US-09-806-382A-3    | Sequence 3, Appli |
| 45 | 73 | 28.2 | 45  | 1 | US-08-056-200-97    | Sequence 97, Appl |

Title: US-10-666-513-2  
 Perfect score: 259  
 Sequence: 1 TKLEDHLEGIINIGHQYSVR.....ELKQLGTHKELPKTLQNXKDQ 50

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|        |       | %     |        |    |                   |                   | Description |
|--------|-------|-------|--------|----|-------------------|-------------------|-------------|
| Result | Query | Match | Length | DB | ID                |                   |             |
| No.    | Score |       |        |    |                   |                   |             |
| 1      | 257   | 99.2  | 50     | 9  | US-09-826-589-2   | Sequence 2, Appli |             |
| 2      | 257   | 99.2  | 50     | 9  | US-09-872-185B-9  | Sequence 9, Appli |             |
| 3      | 257   | 99.2  | 50     | 15 | US-10-666-513-2   | Sequence 2, Appli |             |
| 4      | 257   | 99.2  | 50     | 16 | US-10-665-867-2   | Sequence 2, Appli |             |
| 5      | 230   | 88.8  | 90     | 9  | US-09-826-589-3   | Sequence 3, Appli |             |
| 6      | 230   | 88.8  | 90     | 9  | US-09-826-589-4   | Sequence 4, Appli |             |
| 7      | 230   | 88.8  | 90     | 9  | US-09-872-185B-11 | Sequence 11, Appl |             |
| 8      | 230   | 88.8  | 90     | 9  | US-09-872-185B-12 | Sequence 12, Appl |             |

|    |     |      |     |    |                      |                   |
|----|-----|------|-----|----|----------------------|-------------------|
| 9  | 230 | 88.8 | 90  | 15 | US-10-666-513-3      | Sequence 3, Appli |
| 10 | 230 | 88.8 | 90  | 16 | US-10-665-867-3      | Sequence 3, Appli |
| 11 | 230 | 88.8 | 90  | 16 | US-10-665-867-4      | Sequence 4, Appli |
| 12 | 189 | 73.0 | 92  | 14 | US-10-077-600-2      | Sequence 2, Appli |
| 13 | 189 | 73.0 | 92  | 16 | US-10-755-889-334    | Sequence 334, App |
| 14 | 172 | 66.4 | 46  | 9  | US-09-864-761-41579  | Sequence 41579, A |
| 15 | 114 | 44.0 | 112 | 14 | US-10-205-219-161    | Sequence 161, App |
| 16 | 114 | 44.0 | 113 | 10 | US-09-492-026-7      | Sequence 7, Appli |
| 17 | 110 | 42.5 | 114 | 9  | US-09-214-272-4      | Sequence 4, Appli |
| 18 | 110 | 42.5 | 114 | 14 | US-10-134-841-4      | Sequence 4, Appli |
| 19 | 110 | 42.5 | 114 | 14 | US-10-308-279-32     | Sequence 32, Appl |
| 20 | 110 | 42.5 | 114 | 14 | US-10-116-275-225    | Sequence 225, App |
| 21 | 110 | 42.5 | 114 | 14 | US-10-131-410-146    | Sequence 146, App |
| 22 | 110 | 42.5 | 114 | 15 | US-10-424-599-159736 | Sequence 159736,  |
| 23 | 110 | 42.5 | 114 | 16 | US-10-755-889-330    | Sequence 330, App |
| 24 | 110 | 42.5 | 114 | 17 | US-10-733-969A-49    | Sequence 49, Appl |
| 25 | 109 | 42.1 | 44  | 9  | US-09-864-761-41096  | Sequence 41096, A |
| 26 | 104 | 40.2 | 44  | 10 | US-09-877-843-84     | Sequence 84, Appl |
| 27 | 89  | 34.4 | 101 | 9  | US-09-393-433-2      | Sequence 2, Appli |
| 28 | 89  | 34.4 | 101 | 9  | US-09-781-509-2      | Sequence 2, Appli |
| 29 | 89  | 34.4 | 101 | 14 | US-10-269-643-2      | Sequence 2, Appli |
| 30 | 89  | 34.4 | 119 | 13 | US-10-087-192-1155   | Sequence 1155, Ap |
| 31 | 87  | 33.6 | 95  | 9  | US-09-919-172-102    | Sequence 102, App |
| 32 | 87  | 33.6 | 95  | 9  | US-09-981-353-98     | Sequence 98, Appl |
| 33 | 87  | 33.6 | 95  | 17 | US-10-752-986-102    | Sequence 102, App |
| 34 | 87  | 33.6 | 113 | 15 | US-10-276-774-2377   | Sequence 2377, Ap |
| 35 | 84  | 32.4 | 66  | 15 | US-10-336-603A-104   | Sequence 104, App |
| 36 | 84  | 32.4 | 92  | 10 | US-09-492-026-5      | Sequence 5, Appli |
| 37 | 84  | 32.4 | 92  | 10 | US-09-919-039-184    | Sequence 184, App |
| 38 | 84  | 32.4 | 92  | 15 | US-10-336-603A-102   | Sequence 102, App |
| 39 | 84  | 32.4 | 97  | 16 | US-10-363-829-412    | Sequence 412, App |
| 40 | 84  | 32.4 | 101 | 17 | US-10-425-115-219479 | Sequence 219479,  |
| 41 | 83  | 32.0 | 92  | 17 | US-10-425-115-236005 | Sequence 236005,  |
| 42 | 83  | 32.0 | 101 | 9  | US-09-393-433-1      | Sequence 1, Appli |
| 43 | 83  | 32.0 | 101 | 9  | US-09-781-509-1      | Sequence 1, Appli |
| 44 | 83  | 32.0 | 101 | 13 | US-10-067-618-2      | Sequence 2, Appli |
| 45 | 83  | 32.0 | 101 | 13 | US-10-135-152-2      | Sequence 2, Appli |

Title: US-10-666-513-2  
 Perfect score: 259  
 Sequence: 1 TKLEDHLEGIINIGHQYSVR.....ELKQLGTKELPKTLQN XKDQ 50

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Query |        | DB | ID     | Description        |
|------------|-------|---------|--------|----|--------|--------------------|
|            |       | Match   | Length |    |        |                    |
| 1          | 206   | 79.5    | 91     | 2  | A55406 | calgranulin c - pi |
| 2          | 189   | 73.0    | 92     | 2  | JC4712 | S-100 calcium-bind |
| 3          | 131   | 50.6    | 122    | 1  | A42628 | calgranulin B - bo |
| 4          | 114   | 44.0    | 113    | 1  | JN0686 | calgranulin B - ra |
| 5          | 110   | 42.5    | 114    | 1  | B31848 | calgranulin B [val |
| 6          | 89    | 34.4    | 101    | 2  | S06207 | calvasculin - mous |
| 7          | 87    | 33.6    | 95     | 2  | S24146 | S-100 protein P -  |
| 8          | 87    | 33.6    | 101    | 2  | S01759 | calvasculin - rat  |
| 9          | 84    | 32.4    | 92     | 1  | BCHUIB | S-100 protein beta |
| 10         | 84    | 32.4    | 92     | 2  | A48015 | S-100 protein beta |
| 11         | 84    | 32.4    | 92     | 2  | A26557 | S-100 protein beta |
| 12         | 83    | 32.0    | 91     | 1  | BCBOIB | S-100 protein beta |
| 13         | 83    | 32.0    | 100    | 2  | A53217 | placental calcium- |
| 14         | 83    | 32.0    | 101    | 2  | A48219 | calvasculin - huma |
| 15         | 81    | 31.3    | 591    | 2  | A45135 | profilaggrin - hum |
| 16         | 78    | 30.1    | 113    | 1  | S68242 | calgranulin B - mo |
| 17         | 77    | 29.7    | 306    | 2  | A48118 | major epidermal ca |
| 18         | 74    | 28.6    | 93     | 1  | BCHUCF | calgranulin A [val |
| 19         | 73    | 28.2    | 89     | 1  | I56163 | calgranulin A - mo |
| 20         | 72    | 27.8    | 95     | 1  | S35985 | S-100 protein alph |
| 21         | 71    | 27.4    | 94     | 1  | BCBOIA | S-100 protein alph |
| 22         | 71    | 27.4    | 94     | 1  | BCHUIA | S-100 protein alph |
| 23         | 70    | 27.0    | 89     | 1  | JN0685 | calgranulin A - ra |
| 24         | 69.5  | 26.8    | 110    | 2  | B48219 | S-100 calcium-bind |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 25 | 68   | 26.3 | 90   | 1 | BCHUY  | calcyclin - human  |
| 26 | 68   | 26.3 | 98   | 2 | JC5064 | S-100 calcium-bind |
| 27 | 68   | 26.3 | 98   | 2 | JC5065 | calcium-binding pr |
| 28 | 67   | 25.9 | 90   | 1 | S27011 | calcyclin - rabbit |
| 29 | 67   | 25.9 | 98   | 2 | A41988 | S-100 calcium-bind |
| 30 | 65   | 25.1 | 217  | 2 | JE0330 | 26-kDa Ca2+-bindin |
| 31 | 64   | 24.7 | 89   | 2 | A54314 | calcyclin - mouse  |
| 32 | 64   | 24.7 | 90   | 2 | B28363 | calcyclin - rat    |
| 33 | 64   | 24.7 | 279  | 2 | AI1012 | hypothetical prote |
| 34 | 63.5 | 24.5 | 876  | 2 | G89952 | DNA polymerase I [ |
| 35 | 63   | 24.3 | 102  | 1 | JQ1300 | calgizzarin - rabb |
| 36 | 61.5 | 23.7 | 310  | 2 | AG1733 | gp49 (Bacteriophag |
| 37 | 61   | 23.6 | 97   | 2 | A30129 | S-100 protein, lun |
| 38 | 61   | 23.6 | 469  | 2 | S55167 | IME2-dependent sig |
| 39 | 60.5 | 23.4 | 97   | 1 | JH0663 | calpactin I light  |
| 40 | 60.5 | 23.4 | 438  | 2 | H72241 | fixC protein - The |
| 41 | 58.5 | 22.6 | 97   | 2 | A28489 | calpactin I light  |
| 42 | 57.5 | 22.2 | 283  | 2 | G83754 | transcription regu |
| 43 | 57.5 | 22.2 | 455  | 2 | E90316 | oxidoreductase [im |
| 44 | 57.5 | 22.2 | 757  | 2 | B90572 | lipoprotein [impor |
| 45 | 57.5 | 22.2 | 2108 | 2 | S28417 | CDC39 protein - ye |



Title: US-10-666-513-2  
 Perfect score: 259  
 Sequence: 1 TKLEDHLEGIINIGHQYSVR.....ELKQLGTHKELPKTLQNXXKDQ 50

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181.

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_02:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result |       | %           |        |    |            |                    |  |
|--------|-------|-------------|--------|----|------------|--------------------|--|
| No.    | Score | Query Match | Length | DB | ID         | Description        |  |
| 1      | 230   | 88.8        | 70     | 2  | Q9TR16     | Q9tr16 bos taurus  |  |
| 2      | 230   | 88.8        | 91     | 1  | S112_BOVIN | P79105 bos taurus  |  |
| 3      | 206   | 79.5        | 91     | 1  | S112_PIG   | P80310 sus scrofa  |  |
| 4      | 189   | 73.0        | 91     | 1  | S112_HUMAN | P80511 homo sapien |  |
| 5      | 189   | 73.0        | 92     | 2  | AAH70294   | Aah70294 homo sapi |  |
| 6      | 136   | 52.5        | 81     | 1  | S112_RABIT | O77791 oryctolagus |  |
| 7      | 133   | 51.4        | 122    | 1  | S109_BOVIN | P28783 bos taurus  |  |
| 8      | 114   | 44.0        | 111    | 2  | Q761U7     | Q761u7 rattus norv |  |
| 9      | 114   | 44.0        | 111    | 2  | BAC82423   | Bac82423 rattus no |  |
| 10     | 114   | 44.0        | 112    | 1  | S109_RAT   | P50116 rattus norv |  |
| 11     | 110   | 42.5        | 114    | 1  | S109_HUMAN | P06702 homo sapien |  |
| 12     | 98    | 37.8        | 119    | 2  | Q6PRV2     | Q6prv2 coturnix co |  |
| 13     | 98    | 37.8        | 119    | 2  | AAT01286   | Aat01286 coturnix  |  |
| 14     | 94    | 36.3        | 118    | 1  | S109_RABIT | P50117 oryctolagus |  |
| 15     | 94    | 36.3        | 119    | 1  | M126_CHICK | P28318 gallus gall |  |
| 16     | 91    | 35.1        | 100    | 2  | Q7ZVA4     | Q7zva4 brachydanio |  |
| 17     | 90    | 34.7        | 101    | 2  | O93395     | O93395 salvelinus  |  |
| 18     | 89    | 34.4        | 101    | 1  | S104_MOUSE | P07091 mus musculu |  |
| 19     | 89    | 34.4        | 101    | 2  | BAB22543   | Bab22543 mus muscu |  |
| 20     | 87.5  | 33.8        | 2850   | 1  | HORN_HUMAN | Q86yz3 homo sapien |  |
| 21     | 87    | 33.6        | 95     | 1  | S10P_HUMAN | P25815 homo sapien |  |
| 22     | 87    | 33.6        | 95     | 2  | AAO41114   | Aao41114 homo sapi |  |
| 23     | 87    | 33.6        | 95     | 2  | AAP35953   | Aap35953 homo sapi |  |
| 24     | 87    | 33.6        | 101    | 1  | S104_RAT   | P05942 rattus norv |  |
| 25     | 85    | 32.8        | 92     | 2  | Q925T3     | Q925t3 cricetulus  |  |
| 26     | 84    | 32.4        | 91     | 1  | S10B_HUMAN | P04271 homo sapien |  |

|    |    |      |      |   |            |          |             |           |
|----|----|------|------|---|------------|----------|-------------|-----------|
| 27 | 84 | 32.4 | 91   | 1 | S10B_MOUSE | P50114   | mus         | musculu   |
| 28 | 84 | 32.4 | 91   | 1 | S10B_RAT   | P04631   | rattus      | norv      |
| 29 | 84 | 32.4 | 92   | 2 | Q6YNR6     | Q6ynr6   | oryctolagus |           |
| 30 | 84 | 32.4 | 92   | 2 | AAL12231   | Aal12231 | oryctolag   |           |
| 31 | 84 | 32.4 | 92   | 2 | AAH61178   | Aah61178 | mus         | muscu     |
| 32 | 84 | 32.4 | 95   | 2 | Q6DGT8     | Q6dgt8   | brachydanio |           |
| 33 | 83 | 32.0 | 91   | 1 | S10B_BOVIN | P02638   | bos         | taurus    |
| 34 | 83 | 32.0 | 100  | 1 | S104_BOVIN | P35466   | bos         | taurus    |
| 35 | 83 | 32.0 | 101  | 1 | S104_HUMAN | P26447   | homo        | sapien    |
| 36 | 83 | 32.0 | 101  | 2 | CAG29341   | Cag29341 | homo        | sapi      |
| 37 | 81 | 31.3 | 591  | 2 | Q01720     | Q01720   | homo        | sapien    |
| 38 | 81 | 31.3 | 687  | 2 | Q9H4U2     | Q9h4u2   | homo        | sapien    |
| 39 | 78 | 30.1 | 112  | 1 | S109_MOUSE | P31725   | mus         | musculu   |
| 40 | 77 | 29.7 | 1218 | 2 | Q05331     | Q05331   | homo        | sapien    |
| 41 | 75 | 29.0 | 148  | 2 | Q8BLX1     | Q8blx1   | mus         | musculu   |
| 42 | 75 | 29.0 | 2496 | 1 | HORN_MOUSE | Q8vhd8   | mus         | musculu   |
| 43 | 74 | 28.6 | 93   | 1 | S108_HUMAN | P05109   | h           | calgranul |
| 44 | 74 | 28.6 | 93   | 2 | AAP36042   | Aap36042 | homo        | sapi      |
| 45 | 74 | 28.6 | 93   | 2 | CAG28602   | Cag28602 | homo        | sapi      |